

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/553,730
Source: P4710
Date Processed by STIC: 11/1/05

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PCT

RAW SEQUENCE LISTING

DATE: 11/01/2005

PATENT APPLICATION: US/10/553,730

TIME: 10:49:16

Input Set : A:\SEQUENCE LIST 33157A.TXT

Output Set: N:\CRF4\11012005\J553730.raw

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3 <110> APPLICANT: KUMAR, Chandrika S.
4   DAOUTI, Sherif
5   LATARIO, Brian J.
7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS TARGETING TYROSINE KINASES
9 <130> FILE REFERENCE: 3491/0M582US0
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/553,730
C--> 12 <141> CURRENT FILING DATE: 2005-10-14
14 <160> NUMBER OF SEQ ID NOS: 35
16 <170> SOFTWARE: PatentIn version 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3949
20 <212> TYPE: DNA
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28 ctcccgccagc cctcctccct ccgcgtccct tcccgccgcc tctcctccgc cctcctccct    180
30 cctcgctcgc gggccggggc cggcatgggt cggcgctgcc gccgatggcg ctgaggcgga    240
32 gcatggggcgc gccggggctc ccgccgctgc cgtcgccgcc gccaccggcg ctcgggctgc    300
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48 ctgaacctgt taccattgtc tgggtggagag gaactacgaa gatcggggga cccgctccct    780
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58 caggaggtcg ggaagtcccg gctgttgggt tccctgtgcc cccctttacc tgctgctcc    1080
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82 aaaaactgga ggatgtgctc atcccagagc agcagttcac cctgggccgg atgttgggca 1800
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86 aagtggctgt gaagatgctg aaagctgaca tcattgcctc aagcgacatt gaagagttcc 1920
88 tcagggaagc agcttgcatg aaggagtttg accatccaca cgtggccaaa cttgttgggg 1980
90 taagcctccg gagcagggct aaaggccgtc tccccatccc catggtcatc ttgcccttca 2040
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152 accccagcct tgggtggggg gcctctggaa tgcattgggc gggctcctagc tgttaggggc 3900
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157 <210> SEQ ID NO: 2

158 <211> LENGTH: 890

159 <212> TYPE: PRT

160 <213> ORGANISM: Homo sapiens

162 <400> SEQUENCE: 2

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165 1 5 10 15

168 Leu Pro Pro Pro Pro Arg Leu Gly Leu Leu Leu Ala Ala Leu Ala Ser

169 20 25 30

172 Leu Leu Leu Pro Glu Ser Ala Ala Ala Gly Leu Lys Leu Met Gly Ala

173 35 40 45

176 Pro Val Lys Leu Thr Val Ser Gln Gly Gln Pro Val Lys Leu Asn Cys

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180 Ser Val Glu Gly Met Glu Glu Pro Asp Ile Gln Trp Val Lys Asp Gly
181 65      70      75      80
184 Ala Val Val Gln Asn Leu Asp Gln Leu Tyr Ile Pro Val Ser Glu Gln
185      85      90      95
188 His Trp Ile Gly Phe Leu Ser Leu Lys Ser Val Glu Arg Ser Asp Ala
189      100      105      110
192 Gly Arg Tyr Trp Cys Gln Val Glu Asp Gly Gly Glu Thr Glu Ile Ser
193      115      120      125
196 Gln Pro Val Trp Leu Thr Val Glu Gly Val Pro Phe Phe Thr Val Glu
197      130      135      140
200 Pro Lys Asp Leu Ala Val Pro Pro Asn Ala Pro Phe Gln Leu Ser Cys
201 145      150      155      160
204 Glu Ala Val Gly Pro Pro Glu Pro Val Thr Ile Val Trp Trp Arg Gly
205      165      170      175
208 Thr Thr Lys Ile Gly Gly Pro Ala Pro Ser Pro Ser Val Leu Asn Val
209      180      185      190
212 Thr Gly Val Thr Gln Ser Thr Met Phe Ser Cys Glu Ala His Asn Leu
213      195      200      205
216 Lys Gly Leu Ala Ser Ser Arg Thr Ala Thr Val His Leu Gln Ala Leu
217      210      215      220
220 Pro Ala Ala Pro Phe Asn Ile Thr Val Thr Lys Leu Ser Ser Ser Asn
221 225      230      235      240
224 Ala Ser Val Ala Trp Met Pro Gly Ala Asp Gly Arg Ala Leu Leu Gln
225      245      250      255
228 Ser Cys Thr Val Gln Val Thr Gln Ala Pro Gly Gly Trp Glu Val Leu
229      260      265      270
232 Ala Val Val Val Pro Val Pro Pro Phe Thr Cys Leu Leu Arg Asp Leu
233      275      280      285
236 Val Pro Ala Thr Asn Tyr Ser Leu Arg Val Arg Cys Ala Asn Ala Leu
237      290      295      300
240 Gly Pro Ser Pro Tyr Ala Asp Trp Val Pro Phe Gln Thr Lys Gly Leu
241 305      310      315      320
244 Ala Pro Ala Ser Ala Pro Gln Asn Leu His Ala Ile Arg Thr Asp Ser
245      325      330      335
248 Gly Leu Ile Leu Glu Trp Glu Glu Val Ile Pro Glu Ala Pro Leu Glu
249      340      345      350
252 Gly Pro Leu Gly Pro Tyr Lys Leu Ser Trp Val Gln Asp Asn Gly Thr
253      355      360      365
256 Gln Asp Glu Leu Thr Val Glu Gly Thr Arg Ala Asn Leu Thr Gly Trp
257      370      375      380
260 Asp Pro Gln Lys Asp Leu Ile Val Arg Val Cys Val Ser Asn Ala Val
261 385      390      395      400
264 Gly Cys Gly Pro Trp Ser Gln Pro Leu Val Val Ser Ser His Asp Arg
265      405      410      415
268 Ala Gly Gln Gln Gly Pro Pro His Ser Arg Thr Ser Trp Val Pro Val
269      420      425      430
272 Val Leu Gly Val Leu Thr Ala Leu Val Thr Ala Ala Ala Leu Ala Leu
273      435      440      445

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276 Ile Leu Leu Arg Lys Arg Arg Lys Glu Thr Arg Phe Gly Gln Ala Phe
277      450      455      460
280 Asp Ser Val Met Ala Arg Gly Glu Pro Ala Val His Phe Arg Ala Ala
281 465      470      475      480
284 Arg Ser Phe Asn Arg Glu Arg Pro Glu Arg Ile Glu Ala Thr Leu Asp
285      485      490      495
288 Ser Leu Gly Ile Ser Asp Glu Leu Lys Glu Lys Leu Glu Asp Val Leu
289      500      505      510
292 Ile Pro Glu Gln Gln Phe Thr Leu Gly Arg Met Leu Gly Lys Gly Glu
293      515      520      525
296 Phe Gly Ser Val Arg Glu Ala Gln Leu Lys Gln Glu Asp Gly Ser Phe
297      530      535      540
300 Val Lys Val Ala Val Lys Met Leu Lys Ala Asp Ile Ile Ala Ser Ser
301 545      550      555      560
304 Asp Ile Glu Glu Phe Leu Arg Glu Ala Ala Cys Met Lys Glu Phe Asp
305      565      570      575
308 His Pro His Val Ala Lys Leu Val Gly Val Ser Leu Arg Ser Arg Ala
309      580      585      590
312 Lys Gly Arg Leu Pro Ile Pro Met Val Ile Leu Pro Phe Met Lys His
313      595      600      605
316 Gly Asp Leu His Ala Phe Leu Leu Ala Ser Arg Ile Gly Glu Asn Pro
317      610      615      620
320 Phe Asn Leu Pro Leu Gln Thr Leu Ile Arg Phe Met Val Asp Ile Ala
321 625      630      635      640
324 Cys Gly Met Glu Tyr Leu Ser Ser Arg Asn Phe Ile His Arg Asp Leu
325      645      650      655
328 Ala Ala Arg Asn Cys Met Leu Ala Glu Asp Met Thr Val Cys Val Ala
329      660      665      670
332 Asp Phe Gly Leu Ser Arg Lys Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln
333      675      680      685
336 Gly Cys Ala Ser Lys Leu Pro Val Lys Trp Leu Ala Leu Glu Ser Leu
337      690      695      700
340 Ala Asp Asn Leu Tyr Thr Val Gln Ser Asp Val Trp Ala Phe Gly Val
341 705      710      715      720
344 Thr Met Trp Glu Ile Met Thr Arg Gly Gln Thr Pro Tyr Ala Gly Ile
345      725      730      735
348 Glu Asn Ala Glu Ile Tyr Asn Tyr Leu Ile Gly Gly Asn Arg Leu Lys
349      740      745      750
352 Gln Pro Pro Glu Cys Met Glu Asp Val Tyr Asp Leu Met Tyr Gln Cys
353      755      760      765
356 Trp Ser Ala Asp Pro Lys Gln Arg Pro Ser Phe Thr Cys Leu Arg Met
357      770      775      780
360 Glu Leu Glu Asn Ile Leu Gly Gln Leu Ser Val Leu Ser Ala Ser Gln
361 785      790      795      800
364 Asp Pro Leu Tyr Ile Asn Ile Glu Arg Ala Glu Glu Pro Thr Ala Gly
365      805      810      815
368 Gly Ser Leu Glu Leu Pro Gly Arg Asp Gln Pro Tyr Ser Gly Ala Gly
369      820      825      830
372 Asp Gly Ser Gly Met Gly Ala Val Gly Gly Thr Pro Ser Asp Cys Arg

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373      835      840      845
376 Tyr Ile Leu Thr Pro Gly Gly Leu Ala Glu Gln Pro Gly Gln Ala Glu
377      850      855      860
380 His Gln Pro Glu Ser Pro Leu Asn Glu Thr Gln Arg Leu Leu Leu Leu
381 865      870      875      880
384 Gln Gln Gly Leu Leu Pro His Ser Ser Cys
385      885      890
388 <210> SEQ ID NO: 3
389 <211> LENGTH: 678
390 <212> TYPE: PRT
391 <213> ORGANISM: Homo sapiens
393 <400> SEQUENCE: 3
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396 1      5      10      15
399 Gln Leu Leu Leu Leu Leu Leu Ala Ala Glu Cys Ala Leu Ala Ala Leu
400      20      25      30
403 Leu Pro Ala Arg Glu Ala Thr Gln Phe Leu Arg Pro Arg Gln Arg Arg
404      35      40      45
407 Ala Phe Gln Val Phe Glu Glu Ala Lys Gln Gly His Leu Glu Arg Glu
408      50      55      60
411 Cys Val Glu Glu Leu Cys Ser Arg Glu Glu Ala Arg Glu Val Phe Glu
412 65      70      75      80
415 Asn Asp Pro Glu Thr Asp Tyr Phe Tyr Pro Arg Tyr Leu Asp Cys Ile
416      85      90      95
419 Asn Lys Tyr Gly Ser Pro Tyr Thr Lys Asn Ser Gly Phe Ala Thr Cys
420      100      105      110
423 Val Gln Asn Leu Pro Asp Gln Cys Thr Pro Asn Pro Cys Asp Arg Lys
424      115      120      125
427 Gly Thr Gln Ala Cys Gln Asp Leu Met Gly Asn Phe Phe Cys Leu Cys
428      130      135      140
431 Lys Ala Gly Trp Gly Gly Arg Leu Cys Asp Lys Asp Val Asn Glu Cys
432 145      150      155      160
435 Ser Gln Glu Asn Gly Gly Cys Leu Gln Ile Cys His Asn Lys Pro Gly
436      165      170      175
439 Ser Phe His Cys Ser Cys His Ser Gly Phe Glu Leu Ser Ser Asp Gly
440      180      185      190
443 Arg Thr Cys Gln Asp Ile Asp Glu Cys Ala Asp Ser Glu Ala Cys Gly
444      195      200      205
447 Glu Ala Arg Cys Lys Asn Leu Pro Gly Ser Tyr Ser Cys Leu Cys Asp
448      210      215      220
451 Glu Gly Phe Ala Tyr Ser Ser Gln Glu Lys Ala Cys Arg Asp Val Asp
452 225      230      235      240
455 Glu Cys Leu Gln Gly Arg Cys Glu Gln Val Cys Val Asn Ser Pro Gly
456      245      250      255
459 Ser Tyr Thr Cys His Cys Asp Gly Arg Gly Gly Leu Lys Leu Ser Gln
460      260      265      270
463 Asp Met Asp Thr Cys Glu Asp Ile Leu Pro Cys Val Pro Phe Ser Val
464      275      280      285
467 Ala Lys Ser Val Lys Ser Leu Tyr Leu Gly Arg Met Phe Ser Gly Thr

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date